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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/842,628

DATE: 09/21/2001
TIME: 20:44:39

Input Set : A:\23032108.app
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ENTERED

3 <110> APPLICANT: ROBERTS, JOSEPH
 4 MACALLISTER, THOMAS W.
 5 SETHURAMAN, NATARAJAN
 6 FREEMAN, ABBIE G.
 8 <120> TITLE OF INVENTION: GENETICALLY ENGINEERED GLUTAMINASE AND ITS USE IN
 9 ANTIVIRAL AND ANTICANCER THERAPY
 11 <130> FILE REFERENCE: 023032/0108
 13 <140> CURRENT APPLICATION NUMBER: 09/842,628
 14 <141> CURRENT FILING DATE: 2001-04-27
 16 <150> PRIOR APPLICATION NUMBER: 08/050,482
 17 <151> PRIOR FILING DATE: 1995-04-25
 19 <150> PRIOR APPLICATION NUMBER: PCT/US92/10421
 20 <151> PRIOR FILING DATE: 1992-12-04
 22 <150> PRIOR APPLICATION NUMBER: DE P 4140003.8
 23 <151> PRIOR FILING DATE: 1991-12-04
 25 <160> NUMBER OF SEQ ID NOS: 22
 27 <170> SOFTWARE: PatentIn Ver. 2.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 1014
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Pseudomonas sp.
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (1)..(1008)
 38 <400> SEQUENCE: 1
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 40 Lys Glu Val Glu Asn Gln Gln Lys Leu Ala Asn Val Val Ile Leu Ala
 41 1 5 10 15
 43 acc ggc ggc acc atc gcc ggc gct ggc gcc agc gcg gcc aac agc gcc 96
 44 Thr Gly Gly Thr Ile Ala Gly Ala Gly Ala Ser Ala Ala Asn Ser Ala
 45 20 25 30
 47 acc tac cag gct gcc aag gtt ggc gtc gac aag ctg att gcc ggc gtg 144
 48 Thr Tyr Gln Ala Ala Lys Val Gly Val Asp Lys Leu Ile Ala Gly Val
 49 35 40 45
 51 ccg gag ctg gcc gac ctg gcc aat gtg cgc ggc gag cag gtg atg cag 192
 52 Pro Glu Leu Ala Asp Leu Ala Asn Val Arg Gly Glu Gln Val Met Gln
 53 50 55 60
 55 atc gcc tcc gaa agc atc acc aac gac gac ctg ctc aag ctg gca agc 240
 56 Ile Ala Ser Glu Ser Ile Thr Asn Asp Asp Leu Leu Lys Leu Ala Ser
 57 65 70 75 80
 59 agc gtg gcc gag ctg gcc gac agc aat gac gtc gat ggc atc gtc atc 288
 60 Ser Val Ala Glu Leu Ala Asp Ser Asn Asp Val Asp Gly Ile Val Ile
 61 85 90 95
 63 acc cat ggc acc gac acc ctg gaa gaa acc gcc tac ttt ttg aac ctc 336
 64 Thr His Gly Thr Asp Thr Leu Glu Glu Thr Ala Tyr Phe Leu Asn Leu
 65 100 105 110
 67 gtg gaa aag acc gac aag ccg atc gtc gtg gtc ggt tcc atg cgc ccc 384

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68	Val	Glu	Lys	Thr	Asp	Lys	Pro	Ile	Val	Val	Val	Gly	Ser	Met	Arg	Pro	
69	115							120								125	
71	ggc	acc	gcc	atg	tcc	gcc	gac	ggc	atg	ctc	aac	ctg	tac	aac	gcc	gtg	432
72	Gly	Thr	Ala	Met	Ser	Ala	Asp	Gly	Met	Leu	Asn	Leu	Tyr	Asn	Ala	Val	
73	130							135								140	
75	gcc	gtg	gcc	agc	aac	aag	gac	tcg	cgc	ggc	aag	ggc	gtg	ctg	gtg	acc	480
76	Ala	Val	Ala	Ser	Asn	Lys	Asp	Ser	Arg	Gly	Lys	Gly	Val	Leu	Val	Thr	
77	145							150								160	
79	atg	aac	gac	gag	atc	cag	tcc	ggg	cgt	gac	gtg	agc	aag	tcg	atc	aac	528
80	Met	Asn	Asp	Glu	Ile	Gln	Ser	Gly	Arg	Asp	Val	Ser	Lys	Ser	Ile	Asn	
81		165						170								175	
83	atc	aag	acc	gaa	gcc	tcc	aag	ago	gcc	tgg	ggc	ccg	ctg	ggc	atg	gtg	576
84	Ile	Lys	Thr	Glu	Ala	Phe	Lys	Ser	Ala	Trp	Gly	Pro	Leu	Gly	Met	Val	
85		180						185								190	
87	gtg	gaa	ggc	aag	tcg	tac	tgg	tcc	cgc	ctg	ccg	ggc	aag	cgc	cac	acg	624
88	Val	Glu	Gly	Lys	Ser	Tyr	Trp	Phe	Arg	Leu	Pro	Ala	Lys	Arg	His	Thr	
89		195					200									205	
91	gtc	aac	tcc	qag	tcc	gac	atc	aag	cag	atc	agc	agc	ctg	ccc	cag	gtg	672
92	Val	Asn	Ser	Glu	Phe	Asp	Ile	Lys	Gln	Ile	Ser	Ser	Leu	Pro	Gln	Val	
93		210					215									220	
95	gac	atc	gcc	tac	agc	tat	ggc	aac	gtc	acc	gac	acg	gcc	tac	aag	gcc	720
96	Asp	Ile	Ala	Tyr	Ser	Tyr	Gly	Asn	Val	Thr	Asp	Thr	Ala	Tyr	Lys	Ala	
97	225						230									240	
99	ctg	gca	cag	aac	ggc	aag	gcg	ctg	atc	cat	gcc	ggc	acc	ggc	aat		768
100	Leu	Ala	Gln	Asn	Gly	Ala	Lys	Ala	Leu	Ile	His	Ala	Gly	Thr	Gly	Asn	
101		245					250									255	
103	ggc	tcg	gtg	tcg	tcg	cgg	gtg	gtg	cca	gcc	ctg	cag	gag	ctg	cgc	aag	816
104	Gly	Ser	Val	Ser	Ser	Arg	Val	Val	Pro	Ala	Leu	Gln	Glu	Leu	Arg	Lys	
105		260					265									270	
107	aac	ggc	gtg	cag	atc	att	cgt	tcg	tca	cgt	caa	cag	ggc	ggt	ttc	gtg	864
108	Asn	Gly	Val	Gln	Ile	Ile	Arg	Ser	Ser	Arg	Gln	Gln	Gly	Gly	Phe	Val	
109		275					280									285	
111	ctg	cgt	aac	gcc	gag	cag	ccc	gac	gac	aag	aac	gac	tgg	gtc	gtg	gcc	912
112	Leu	Arg	Asn	Ala	Glu	Gln	Pro	Asp	Asp	Lys	Asn	Asp	Trp	Val	Val	Ala	
113		290					295									300	
115	cac	gac	ctg	aac	ccg	cag	aag	gcc	cgc	atc	ctg	gcg	atg	gtg	gca	atg	960
116	His	Asp	Leu	Asn	Pro	Gln	Lys	Ala	Arg	Ile	Leu	Ala	Met	Val	Ala	Met	
117	305						310									320	
119	acc	aag	acc	cag	gac	agc	aag	gag	ctg	cag	cgc	att	ttc	tgg	gaa	tac	1008
120	Thr	Lys	Thr	Gln	Asp	Ser	Lys	Glu	Leu	Gln	Arg	Ile	Phe	Trp	Glu	Tyr	
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123	tgataa															1014	
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128	<212>	TYPE:	PRT														
129	<213>	ORGANISM:	Pseudomonas sp.														
131	<400>	SEQUENCE:	2														
132	Lys	Glu	Val	Glu	Asn	Gln	Gln	Lys	Leu	Ala	Asn	Val	Val	Ile	Leu	Ala	
133	1						5					10				15	

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135 Thr Gly Gly Thr Ile Ala Gly Ala Gly Ala Ser Ala Ala Asn Ser Ala
 136 20 25 30
 138 Thr Tyr Gln Ala Ala Lys Val Gly Val Asp Lys Leu Ile Ala Gly Val
 139 35 40 45
 141 Pro Glu Leu Ala Asp Leu Ala Asn Val Arg Gly Glu Gln Val Met Gln
 142 50 55 60
 144 Ile Ala Ser Glu Ser Ile Thr Asn Asp Asp Leu Leu Lys Leu Ala Ser
 145 65 70 75 80
 147 Ser Val Ala Glu Leu Ala Asp Ser Asn Asp Val Asp Gly Ile Val Ile
 148 85 90 95
 150 Thr His Gly Thr Asp Thr Leu Glu Glu Thr Ala Tyr Phe Leu Asn Leu
 151 100 105 110
 153 Val Glu Lys Thr Asp Lys Pro Ile Val Val Val Gly Ser Met Arg Pro
 154 115 120 125
 156 Gly Thr Ala Met Ser Ala Asp Gly Met Leu Asn Leu Tyr Asn Ala Val
 157 130 135 140
 159 Ala Val Ala Ser Asn Lys Asp Ser Arg Gly Lys Gly Val Leu Val Thr
 160 145 150 155 160
 162 Met Asn Asp Glu Ile Gln Ser Gly Arg Asp Val Ser Lys Ser Ile Asn
 163 165 170 175
 165 Ile Lys Thr Glu Ala Phe Lys Ser Ala Trp Gly Pro Leu Gly Met Val
 166 180 185 190
 168 Val Glu Gly Lys Ser Tyr Trp Phe Arg Leu Pro Ala Lys Arg His Thr
 169 195 200 205
 171 Val Asn Ser Glu Phe Asp Ile Lys Gln Ile Ser Ser Leu Pro Gln Val
 172 210 215 220
 174 Asp Ile Ala Tyr Ser Tyr Gly Asn Val Thr Asp Thr Ala Tyr Lys Ala
 175 225 230 235 240
 177 Leu Ala Gln Asn Gly Ala Lys Ala Leu Ile His Ala Gly Thr Gly Asn
 178 245 250 255
 180 Gly Ser Val Ser Ser Arg Val Val Pro Ala Leu Gln Glu Leu Arg Lys
 181 260 265 270
 183 Asn Gly Val Gln Ile Ile Arg Ser Ser Arg Gln Gln Gly Gly Phe Val
 184 275 280 285
 186 Leu Arg Asn Ala Glu Gln Pro Asp Asp Lys Asn Asp Trp Val Val Ala
 187 290 295 300
 189 His Asp Leu Asn Pro Gln Lys Ala Arg Ile Leu Ala Met Val Ala Met
 190 305 310 315 320
 192 Thr Lys Thr Gln Asp Ser Lys Glu Leu Gln Arg Ile Phe Trp Glu Tyr
 193 325 330 335
 196 <210> SEQ ID NO: 3
 197 <211> LENGTH: 20
 198 <212> TYPE: DNA
 199 <213> ORGANISM: Artificial Sequence
 201 <220> FEATURE:
 202 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 204 <400> SEQUENCE: 3
 205 tgcagcttga gcaggctcgtc 20
 208 <210> SEQ ID NO: 4

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Input Set : A:\23032108.app
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209 <211> LENGTH: 21
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
216 <400> SEQUENCE: 4
217 ctggccgacc tggccaatgt g 21
220 <210> SEQ ID NO: 5
221 <211> LENGTH: 20
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
228 <400> SEQUENCE: 5
229 cctactttt gaacctcgta 20
232 <210> SEQ ID NO: 6
233 <211> LENGTH: 20
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
240 <400> SEQUENCE: 6
241 caagtctgtac tggttccgcc 20
244 <210> SEQ ID NO: 7
245 <211> LENGTH: 21
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
252 <400> SEQUENCE: 7
253 caatcgtcct ggcgactcggt g 21
256 <210> SEQ ID NO: 8
257 <211> LENGTH: 20
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
264 <400> SEQUENCE: 8
265 gcagatcatt cgttcgcca 20
268 <210> SEQ ID NO: 9
269 <211> LENGTH: 20
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
276 <400> SEQUENCE: 9
277 tgacgatgcc atcgacgtca 20
280 <210> SEQ ID NO: 10
281 <211> LENGTH: 20

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Input Set : A:\23032108.app
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282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
288 <400> SEQUENCE: 10
289 tcacgtcacg cccggactgg 20
292 <210> SEQ ID NO: 11
293 <211> LENGTH: 20
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
300 <400> SEQUENCE: 11 20
301 agctcctgca gggctggcac
304 <210> SEQ ID NO: 12
305 <211> LENGTH: 14
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
312 <220> FEATURE:
313 <221> NAME/KEY: modified_base
314 <222> LOCATION: (9)
315 <223> OTHER INFORMATION: a, t, c, g, other or unknown
317 <400> SEQUENCE: 12
318 aargargtg araa 14
321 <210> SEQ ID NO: 13
322 <211> LENGTH: 18
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
329 <400> SEQUENCE: 13 18
330 atggaygayg arathgar
333 <210> SEQ ID NO: 14
334 <211> LENGTH: 14
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial Sequence
338 <220> FEATURE:
339 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
341 <400> SEQUENCE: 14
342 athttytgaa 14
345 <210> SEQ ID NO: 15
346 <211> LENGTH: 35
347 <212> TYPE: DNA
348 <213> ORGANISM: Artificial Sequence
350 <220> FEATURE:
351 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
353 <400> SEQUENCE: 15

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/842,628

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Input Set : A:\23032108.app
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L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12